

Amendments to Claims

Claim 1.(Currently Amended) A method for determining gene function between at least two genome-registered collections comprising:

- (a) providing a microorganism comprising genomic DNA;
(ba) assembling at least two one first genome-wide scale, genome-registered collections from the genomic DNA of the microorganism of (a) comprising a collection of reporter gene fusions each fusion comprising a reporter gene operably linked to a genomic DNA fragment. and assembling at least one second genome-wide scale, genome-registered collection from the genomic DNA of the microorganism of (a) which is not a collection of reporter gene fusions ;
(cb) perturbing each collection from (ba) with at least one perturbation;
(de) measuring the response of each collection to each perturbation of (cb); and
(e) analyzing the results of the at least one perturbation to identify patterns of similarities and differences between the at least two genome-registered collections resulting in the determination of gene function.

Claim 2 (Currently Amended) A method according to Claim 1 wherein the perturbation is the result of ~~selected from the group consisting of radiation, humidity, alterations in temperature, alterations in carbon source, alterations in energy source, alterations in nitrogen source, alterations in phosphorus source, alterations in sulfur source, alterations in trace element sources, a change in pH, the presence other organisms, the presence of chemicals, the presence of toxins, and abnormal levels of normal metabolites.~~

Claims 3-8 (Canceled)

Claim 9 (Currently Amended) A method according to ~~any one of Claims 1, 3, 5, 7 or 8~~ wherein the organism-microorganism is selected from the group consisting of prokaryotes and fungi.

Claim 10 (Currently Amended) A method according to Claim 9 wherein the prokaryote is an enteric bacterium.

Claim 11 (Currently Amended) A method according to Claim 10 wherein the enteric bacterium are is selected from the group consisting of *Escherichia* and *Salmonella*.

Claim 12 (Currently Amended) A method according to ~~one of Claims 1, 3, 5, 7 or 8~~ wherein the reporter gene ~~or reporter gene complex~~ is selected from the group consisting of *luxCDABE*, *lacZ*, *gfp*, *cat*, *galK*, *inaZ*, *luc*, *luxAB*, *bgaB*, *nptII*, *phoA*, *uidA* and *xylE*.

Claim 13 (Currently Amended) A method according to ~~one of Claims 1, 3, 5, 7 or 8~~ wherein at least 50% of the ~~genomic nucleotides sequences~~ sequences of the genomic DNA are is known.

Claims 14-22 (Canceled)